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RAW SEQUENCE LISTING

DATE: 09/03/2002

PATENT APPLICATION: US/09/509,738C

TIME: 15:27:32

Input Set : A:\2186PB-1.ST25.txt

Output Set: N:\CRF4\09032002\I509738C.raw

3 <110> APPLICANT: Blatt, Michael
4 Leyman, Barbara
6 <120> TITLE OF INVENTION: Protein Involved in Absciscic Acid Signalling
8 <130> FILE REFERENCE: 2186PB-1
10 <140> CURRENT APPLICATION NUMBER: 09/509,738C
C--> 11 <141> CURRENT FILING DATE: 2000-05-24
13 <160> NUMBER OF SEQ ID NOS: 44
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1205
19 <212> TYPE: DNA
20 <213> ORGANISM: Nicotiana tabacum
22 <220> FEATURE:
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24 <222> LOCATION: (18)..(917)
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29 1 5 10
31 ttc aga gct gac gat caa tcg gac tct cac gcc ata gaa atg gga gac 98
32 Phe Arg Ala Asp Asp Gln Ser Asp Ser His Ala Ile Glu Met Gly Asp
33 15 20 25
35 att act ggc gga gtc aat ctc gac aaa ttc ttc gaa gat gtt gaa gcc 146
36 Ile Thr Gly Gly Val Asn Leu Asp Lys Phe Phe Glu Asp Val Glu Ala
37 30 35 40
39 att aaa gac gaa ctc aaa ggc ctc gag aaa atc tat tcc caa ctc caa 194
40 Ile Lys Asp Glu Leu Lys Gly Leu Glu Lys Ile Tyr Ser Gln Leu Gln
41 45 50 55
43 tct tcc cat gaa aaa agc aag act ctt cac aac gct aaa gcc gtt aaa 242
44 Ser Ser His Glu Lys Ser Lys Thr Leu His Asn Ala Lys Ala Val Lys
45 60 65 70 75
47 gat cta aga tcc aac atg gat aat gac gtt tcc atg gca ttg aag aaa 290
48 Asp Leu Arg Ser Asn Met Asp Asn Asp Val Ser Met Ala Leu Lys Lys
49 80 85 90
51 gcc aaa ttc atc aaa gtt cgt ctc gaa gcc tta gac aga tca aat gca 338
52 Ala Lys Phe Ile Lys Val Arg Leu Glu Ala Leu Asp Arg Ser Asn Ala
53 95 100 105
55 gcg aat cga agc ctc cct gga tgt gga ccc gga agt tca tct gac agg 386
56 Ala Asn Arg Ser Leu Pro Gly Cys Gly Pro Gly Ser Ser Ser Asp Arg
57 110 115 120
59 acg aga act tca gtt gtg aac gga tta agg aag aaa ctt caa gag tca 434
60 Thr Arg Thr Ser Val Val Asn Gly Leu Arg Lys Lys Leu Gln Glu Ser
61 125 130 135

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63 atg aat cag ttc aac gag cta agg caa aag atg gca tct gaa tat agg      482
64 Met Asn Gln Phe Asn Glu Leu Arg Gln Lys Met Ala Ser Glu Tyr Arg
65 140                               145                               150                               155
67 gaa aca gtt caa cga cga tat tat acc gtc aca gga gaa aat cct gat      530
68 Glu Thr Val Gln Arg Arg Tyr Tyr Thr Val Thr Gly Glu Asn Pro Asp
69                               160                               165                               170
71 gaa gca gtt ctt gat aca ctc ata tct aca ggt caa agt gag acg ttc      578
72 Glu Ala Val Leu Asp Thr Leu Ile Ser Thr Gly Gln Ser Glu Thr Phe
73                               175                               180                               185
75 ttg caa aag gca att caa gag caa ggg aga gga caa gtg atg gat aca      626
76 Leu Gln Lys Ala Ile Gln Glu Gln Gly Arg Gly Gln Val Met Asp Thr
77                               190                               195                               200
79 gtt atg gaa att caa gaa agg cat gaa gct gtg aag gaa ttg gag agg      674
80 Val Met Glu Ile Gln Glu Arg His Glu Ala Val Lys Glu Leu Glu Arg
81                               205                               210                               215
83 aat ttg aaa gaa ttg cat caa gta ttc ttg gac atg gct gtt ttg gtt      722
84 Asn Leu Lys Glu Leu His Gln Val Phe Leu Asp Met Ala Val Leu Val
85 220                               225                               230                               235
87 gaa agt caa gga gct caa ctt gat gat att gag agc caa gtg aat agg      770
88 Glu Ser Gln Gly Ala Gln Leu Asp Asp Ile Glu Ser Gln Val Asn Arg
89                               240                               245                               250
91 gct aat tcc ttc gtt aga ggg ggt gct cag caa ctg caa gtg gca agg      818
92 Ala Asn Ser Phe Val Arg Gly Gly Ala Gln Gln Leu Gln Val Ala Arg
93                               255                               260                               265
95 aag cac cag aag aac act aga aaa tgg act tgt ttt gct att att ctt      866
96 Lys His Gln Lys Asn Thr Arg Lys Trp Thr Cys Phe Ala Ile Ile Leu
97                               270                               275                               280
99 ctg ctt atc atc att ttg gtg gtg gtt ctt tct att cag cca tgg aaa      914
100 Leu Leu Ile Ile Ile Leu Val Val Val Leu Ser Ile Gln Pro Trp Lys
101                               285                               290                               295
103 aaa tgagaatttg totatggtca aaggtotttct ggtggacccc ttcaatgttt      967
104 Lys
105 300
107 tgaatattct aaatttttat attttattat tttagccatg cttattattt tgtgttattt      1027
109 tggatttttt ttttgttttt aatgtgggga agagtaaact ggatgggggt ccatgtgcta      1087
111 ttttagagaaa tacttgggag ttctcttttt gtaattattg ctgtatttag agtataattc      1147
113 tttttctata ttgttggcag gttaatttgt ttgtttgatt atattctcat ttagattt      1205
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117 <211> LENGTH: 300
118 <212> TYPE: PRT
119 <213> ORGANISM: Nicotiana tabacum
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128                               20                               25                               30
131 Asn Leu Asp Lys Phe Phe Glu Asp Val Glu Ala Ile Lys Asp Glu Leu
132                               35                               40                               45
135 Lys Gly Leu Glu Lys Ile Tyr Ser Gln Leu Gln Ser Ser His Glu Lys

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136      50      55      60
139 Ser Lys Thr Leu His Asn Ala Lys Ala Val Lys Asp Leu Arg Ser Asn
140 65      70      75      80
143 Met Asp Asn Asp Val Ser Met Ala Leu Lys Lys Ala Lys Phe Ile Lys
144      85      90      95
147 Val Arg Leu Glu Ala Leu Asp Arg Ser Asn Ala Ala Asn Arg Ser Leu
148      100      105      110
151 Pro Gly Cys Gly Pro Gly Ser Ser Ser Asp Arg Thr Arg Thr Ser Val
152      115      120      125
155 Val Asn Gly Leu Arg Lys Lys Leu Gln Glu Ser Met Asn Gln Phe Asn
156      130      135      140
159 Glu Leu Arg Gln Lys Met Ala Ser Glu Tyr Arg Glu Thr Val Gln Arg
160 145      150      155      160
163 Arg Tyr Tyr Thr Val Thr Gly Glu Asn Pro Asp Glu Ala Val Leu Asp
164      165      170      175
167 Thr Leu Ile Ser Thr Gly Gln Ser Glu Thr Phe Leu Gln Lys Ala Ile
168      180      185      190
171 Gln Glu Gln Gly Arg Gly Gln Val Met Asp Thr Val Met Glu Ile Gln
172      195      200      205
175 Glu Arg His Glu Ala Val Lys Glu Leu Glu Arg Asn Leu Lys Glu Leu
176      210      215      220
179 His Gln Val Phe Leu Asp Met Ala Val Leu Val Glu Ser Gln Gly Ala
180 225      230      235      240
183 Gln Leu Asp Asp Ile Glu Ser Gln Val Asn Arg Ala Asn Ser Phe Val
184      245      250      255
187 Arg Gly Gly Ala Gln Gln Leu Gln Val Ala Arg Lys His Gln Lys Asn
188      260      265      270
191 Thr Arg Lys Trp Thr Cys Phe Ala Ile Ile Leu Leu Leu Ile Ile Ile
192      275      280      285
195 Leu Val Val Val Leu Ser Ile Gln Pro Trp Lys Lys
196      290      295      300
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200 <211> LENGTH: 1334
201 <212> TYPE: DNA
202 <213> ORGANISM: Arabidopsis thaliana
204 <220> FEATURE:
205 <221> NAME/KEY: CDS
206 <222> LOCATION: (77)..(991)
208 <400> SEQUENCE: 3
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211 atttttcgaa ttttaa atg aac gat ttg ttt tcc agc tca ttc tct cgc ttc 112
212      Met Asn Asp Leu Phe Ser Ser Ser Phe Ser Arg Phe
213      1      5      10
215 cgc agc gga gaa cca tcc cct cgc cga gac gtt gcc ggc ggt ggc gac 160
216 Arg Ser Gly Glu Pro Ser Pro Arg Arg Asp Val Ala Gly Gly Gly Asp
217      15      20      25
219 gga gtt cag atg gcg aat ccc gcg gga tca acc ggt ggt gtg aac ctc 208
220 Gly Val Gln Met Ala Asn Pro Ala Gly Ser Thr Gly Gly Val Asn Leu
221      30      35      40

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223	gac aag ttc ttc gaa gat gtt gaa tct gtg aaa gaa gag cta aag gag	256
224	Asp Lys Phe Phe Glu Asp Val Glu Ser Val Lys Glu Glu Leu Lys Glu	
225	45 50 55 60	
227	cta gat cgg ctc aac gaa aca ctc tct tca tgt cac gag cag agc aag	304
228	Leu Asp Arg Leu Asn Glu Thr Leu Ser Ser Cys His Glu Gln Ser Lys	
229	65 70 75	
231	acg ctt cac aat gct aaa gcc gtt aaa gat ctc cgg tct aaa atg gac	352
232	Thr Leu His Asn Ala Lys Ala Val Lys Asp Leu Arg Ser Lys Met Asp	
233	80 85 90	
235	ggt gac gtt gga gtc gcg ttg aag aag gcg aag atg att aaa gtt aaa	400
236	Gly Asp Val Gly Val Ala Leu Lys Lys Ala Lys Met Ile Lys Val Lys	
237	95 100 105	
239	ctc gag gcg cta gat cgt gcc aat gct gct aat cgg agt ctc cct ggc	448
240	Leu Glu Ala Leu Asp Arg Ala Asn Ala Ala Asn Arg Ser Leu Pro Gly	
241	110 115 120	
243	tgt gga cct ggt tct tcc tcc gat cga acc agg acc tct gtc ctc aat	496
244	Cys Gly Pro Gly Ser Ser Ser Asp Arg Thr Arg Thr Ser Val Leu Asn	
245	125 130 135 140	
247	ggt ctc agg aag aaa ttg atg gac tct atg gat agt ttc aac cga ttg	544
248	Gly Leu Arg Lys Lys Leu Met Asp Ser Met Asp Ser Phe Asn Arg Leu	
249	145 150 155	
251	agg gag ctt atc tcg tcc gag tat aga gaa act gta cag agg agg tac	592
252	Arg Glu Leu Ile Ser Ser Glu Tyr Arg Glu Thr Val Gln Arg Arg Tyr	
253	160 165 170	
255	ttc acc gtc acc ggc gag aat ccg gat gaa cga acc cta gat cga ctg	640
256	Phe Thr Val Thr Gly Glu Asn Pro Asp Glu Arg Thr Leu Asp Arg Leu	
257	175 180 185	
259	att tcc act gga gag agt gag aga ttc ttg cag aaa gca ata caa gaa	688
260	Ile Ser Thr Gly Glu Ser Glu Arg Phe Leu Gln Lys Ala Ile Gln Glu	
261	190 195 200	
263	caa gga aga gga agg gtg tta gac acc att aac gag att caa gaa agg	736
264	Gln Gly Arg Gly Arg Val Leu Asp Thr Ile Asn Glu Ile Gln Glu Arg	
265	205 210 215 220	
267	cat gat cgc gtt aaa gac att gag aag aat ctc agg gag ctt cac cag	784
268	His Asp Arg Val Lys Asp Ile Glu Lys Asn Leu Arg Glu Leu His Gln	
269	225 230 235	
271	gtg ttt cta gac atg gcc gtg ctg gta gag cac cag gga gct cag ctt	832
272	Val Phe Leu Asp Met Ala Val Leu Val Glu His Gln Gly Ala Gln Leu	
273	240 245 250	
275	gat gac atc gag agt cat gtg ggt cga gct agc tcc ttt atc aga ggc	880
276	Asp Asp Ile Glu Ser His Val Gly Arg Ala Ser Ser Phe Ile Arg Gly	
277	255 260 265	
279	gga act gac cag cta caa acc gct cgg gtt tac cag aag aac acg cga	928
280	Gly Thr Asp Gln Leu Gln Thr Ala Arg Val Tyr Gln Lys Asn Thr Arg	
281	270 275 280	
283	aaa tgg aca tgt att gcc att att att ctc atc atc atc ata act gtt	976
284	Lys Trp Thr Cys Ile Ala Ile Ile Ile Leu Ile Ile Ile Ile Thr Val	
285	285 290 295 300	
287	gtg gtt ctt gct gtt ttaaaaccgt ggaacaacag cagtggcggc ggcggcggtg	1031

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288 Val Val Leu Ala Val
289                               305
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293 ctcaggcaag gcgtctattg cgttgaagtt gaagttgaag ttgagtttcg ttatttgcat 1151
295 atatattctt tctttgaaaa accttattat caaaccagct ttgtgttact actttctact 1211
297 gctggtttgt tgtaaatctc ccgtttatct ggtttttgtg aaagaattta aaatgtgggt 1271
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305 <211> LENGTH: 305
306 <212> TYPE: PRT
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316                               20                               25                               30
319 Ala Asn Pro Ala Gly Ser Thr Gly Gly Val Asn Leu Asp Lys Phe Phe
320                               35                               40                               45
323 Glu Asp Val Glu Ser Val Lys Glu Glu Leu Lys Glu Leu Asp Arg Leu
324                               50                               55                               60
327 Asn Glu Thr Leu Ser Ser Cys His Glu Gln Ser Lys Thr Leu His Asn
328 65                               70                               75                               80
331 Ala Lys Ala Val Lys Asp Leu Arg Ser Lys Met Asp Gly Asp Val Gly
332                               85                               90                               95
335 Val Ala Leu Lys Lys Ala Lys Met Ile Lys Val Lys Leu Glu Ala Leu
336                               100                              105                              110
339 Asp Arg Ala Asn Ala Ala Asn Arg Ser Leu Pro Gly Cys Gly Pro Gly
340                               115                              120                              125
343 Ser Ser Ser Asp Arg Thr Arg Thr Ser Val Leu Asn Gly Leu Arg Lys
344                               130                              135                              140
347 Lys Leu Met Asp Ser Met Asp Ser Phe Asn Arg Leu Arg Glu Leu Ile
348 145                              150                              155                              160
351 Ser Ser Glu Tyr Arg Glu Thr Val Gln Arg Arg Tyr Phe Thr Val Thr
352                               165                              170                              175
355 Gly Glu Asn Pro Asp Glu Arg Thr Leu Asp Arg Leu Ile Ser Thr Gly
356                               180                              185                              190
359 Glu Ser Glu Arg Phe Leu Gln Lys Ala Ile Gln Glu Gln Gly Arg Gly
360                               195                              200                              205
363 Arg Val Leu Asp Thr Ile Asn Glu Ile Gln Glu Arg His Asp Arg Val
364                               210                              215                              220
367 Lys Asp Ile Glu Lys Asn Leu Arg Glu Leu His Gln Val Phe Leu Asp
368 225                              230                              235                              240
371 Met Ala Val Leu Val Glu His Gln Gly Ala Gln Leu Asp Asp Ile Glu
372                               245                              250                              255
375 Ser His Val Gly Arg Ala Ser Ser Phe Ile Arg Gly Gly Thr Asp Gln
376                               260                              265                              270
379 Leu Gln Thr Ala Arg Val Tyr Gln Lys Asn Thr Arg Lys Trp Thr Cys
380                               275                              280                              285

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date